AFFYMETRIX

2004 Affymetrix User Group Meetings

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Full Record

Details for HUGENEFL:X74801_AT
Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	X74801_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	X74801
Sequence Type	Exemplar sequence
Representative Public ID	X74801 NCBI
Target Description	X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence, 1636-1837, H.sapiens Cctg mRNA for chaperonin

Genomic Alignment of Target Sequence

Assembly	April 2003 (NCBI 33)

	Position	% Identity	Cytoband
Alignment(s)	chr1: 153495555-153497649 (-) UCSC	100	q22

	Representative Transcript	UniGene Description	Position
Overlapping Transcripts	NM_005998 NCBI	chaperonin containing TCP1, subunit 3 (gamma)	chr1:153495551-153524840 (-) UCSC

Public Domain and Genome References

Gene Title	chaperonin containing TCP1, subunit 3 (gamma)
Gene Symbol	CCT3 HGNC
Chromosomal Location	1q23
UniGene ID	Hs.1708 NCBI (FULL LENGTH)
Ensembl	ENSG00000163468 Ensembl
LocusLink	7203 NCBI
SwissProt	AAH06501 EMBL-EBI P49368 EMBL-EBI
OMIM	600114 NCBI
RefSeq Protein ID	NP_005989 NCBI

	RefSeq Transcript ID		RefSeq Title	
RefSeq	NM_005998 NCBI		chaperonin containing TCP1, subunit 3 (gamma)	

Functional Annotations

	ID	Title	Organism	Type
	ATH1-121501:246830_AT	chaperonin, putative	Arabidopsis	Putative Ortholog
	ATGENOME1:18906_AT	chaperonin, putative	Arabidopsis	Putative Ortholog
	DROSGENOME1:153982_AT		Drosophila	Putative Ortholog
	MG-U74AV2:161238_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MG-U74AV2:98153_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MG-U74CV2:171548_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOE430A:1459987_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
Ortholog	MU11KSUBA:C79428_RC_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MU11KSUBA:L20509_F_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430_2:1459987_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1416024_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1426067_X_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1448178_A_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1449645_S_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	MOUSE430A_2:1451915_AT	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog

MOUSE430A_2:1459987_S_AT   chaperonin subunit 3 Mouse (gamma)   Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6457	protein folding	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5829	cytosol	not recorded	QuickGO AmiGO
5856	cytoskeleton	traceable author statement	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3754	chaperone activity	traceable author statement	QuickGO AmiGO
5524	ATP binding	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	33873532		0.0
blast	31542292	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring complex, polypeptide 5 [Homo sapiens]	0.0

Protein Domains

Database	ID	Description	E-Value
scop	d1a6da3	d1a6da3 SCOP:d.56.1.2:| Thermosome	4.08E-25
scop	d1gmla_	d1gmla_ SCOP:c.8.5.2:| Thermosome	1.01E-57
scop	d1a6da1	d1a6da1 SCOP:a.129.1.2:| Thermosome	4.81E-83
pfam	cpn60_TCP1	TCP-1/cpn60 chaperonin family	5.7E-210
InterPro	IPR002423 EMBL-EBI	Chaperonin Cpn60/TCP-1	
InterPro	IPR001844 EMBL-EBI	Chaperonin Cpn60	
InterPro	IPR002194 EMBL-EBI	Chaperonin TCP-1	
InterPro	IPR008950 EMBL-EBI	GroEL-like chaperone, ATPase	

Sequence

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>HUGENEFL:X74801_AT
atgactggtgtggaacaatggccatacagggctgttgcccaggccctagaggtcattcct
cgtaccctgatccagaactgtggggccagcaccatccgtctacttacctcccttcgggcc
aagcacacccaggagaactgtgagacctggggtgtaaatggtgagacgggtactttggtg
gacatgaaggaactgggcatatgggagccattggctgtgaagctgcagacttataagaca
gcagtggagacggcagttctgctactgcgaattgatgacatcgtttcaggccacaaaaag
aaaggcgatgaccagagccggcaaggcggggctcctgatgctggccaggagtgagtgcta
ggcaaggctacttcaatgcacagaaccagcagagtctcccctttcctgagccagagtgc
caggaacactgtggacgtctttgttcagaagggatcaggttggggggcagcccccagtcc
ctttctgtcccagctcagttttccaaaagacactgacatgtaattcttctctattgtaag
gtttccatttagtttgcttccgatgattaaatctaagtca
```

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness

Probe Info

ATGACTGGTGTGGAACAATGGCCAT	60	345	1294	Antisense
GAACAATGGCCATACAGGGCTGTTG	61	345	1306	Antisense
CTGATCCAGAACTGTGGGGCCAGCA	62	345	1360	Antisense
CAGAACTGTGGGGCCAGCACCATCC	63	345	1366	Antisense
TGTGGGGCCAGCACCATCCGTCTAC	64	345	1372	Antisense
CTGGGCATATGGGAGCCATTGGCTG	65	345	1486	Antisense
ATATGGGAGCCATTGGCTGTGAAGC	66	345	1492	Antisense
GAGCCATTGGCTGTGAAGCTGCAGA	67	345	1498	Antisense
TTGGCTGTGAAGCTGCAGACTTATA	68	345	1504	Antisense
GAGACGGCAGTTCTGCTACTGCGAA	69	345	1540	Antisense
GCAGTTCTGCTACTGCGAATTGATG	70	345	1546	Antisense
ATTGATGACATCGTTTCAGGCCACA	71	345	1564	Antisense
GTGCTAGGCAAGGCTACTTCAATGC	72	345	1648	Antisense
GGCAAGGCTACTTCAATGCACAGAA	73	345	1654	Antisense
GCTACTTCAATGCACAGAACCAGCA	74	345	1660	Antisense
CACAGAACCAGCAGAGTCTCCCCTT	75	345	1672	Antisense
GAGCCAGAGTGCCAGGAACACTGTG	76	345	1702	Antisense
CACTGACATGTAATTCTTCTCTATT	77	345	1804	Antisense
TAGTTTGCTTCCGATGATTAAATCT	78	345	1843	Antisense
GCTTCCGATGATTAAATCTAAGTCA	79	345	1849	Antisense

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